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AMSH1 -----MFOHTVVSLSPEERVPLSKLGNITISEDITPRR 35
AMSH2 MOQ PFTTVNSLAKKLAMEDPRTVVSLSPEERVPLSKLGNITISEDITPRR 50
AMSH -----SDHGEVVSLLPEDVRVALSQLGSAAVVEDIPFR 35
      *..* ****.*;*****;.. .|.***.*
AMSH1 YRSGVEMERMASVYLEEGNLENAFVLYNKJITLFEVKLPHHRDQQCAV 85
AMSH2 YRSGVEMERMASVYLEEGNLENAFVLYNKJITLFEVKLPHHRDQQCAV 100
AMSH YRSGVKLIIRMASIYSEEGNLEHATIDLNKJITLFEVKLPHHRDXXSAVI 85
      *****; ****;2 ****;1;2;222;*****;*****;****;...|
AMSH1 PEKQDIDMKLKEIAFPRTDELKNDLLKXVYVEYQEVYIQSKNYKAEILKK 135
AMSH2 PEKQDIDMKLKEIAFPRTDELKNDLLKXVYVEYQEVYIQSKNYKAEILKK 150
AMSH PEKQDITVKRLKEIAFPKAEELKAEILKRYTYKEYTYEYNEKKKEAEILKH 135
      ***;* *****;|;***;****;* ..** ..|..* *|..|
AMSH1 LEHQRLIEAKPKRIAQMROOQLESEQFLFEEDQLKKQELARGQMSQOTS 185
AMSH2 LEHQRLIEAKPKRIAQMROOQLESEQFLFEEDQLKKQELARGQMSQOTS 200
AMSH MAIQQELEKEKQRYAQQKQOQLEQEQPHATEEMIRNQELEKERLKIWEF 185
      |..* ..* ..|..* ..* *****.* **; ..|..* ..|..|
AMSH1 G-LSEQIDGSALSCTS--THQNNSLINWFAQQPNKSDATNYASHSPFVNR 232
AMSH2 G-LSEQIDGSALSCTS--THQNNSLINWFAQQPNKSDATNYASHSPFVNR 247
AMSH GKWDPSLGGELVPLDLEKPSLDVFTLTVSSIQFSDCHTIVRAKPFVVD 235
      *..|.1.*.2..|. . . *..* |*...|* ..|..* ..|..*
AMSH1 AITPAATLSAVQNLVVEGLRCVVLPEDLCHKFLQLAESNIVRGIIICGIL 282
AMSH2 AITPAATLSAVQNLVVEGLRCVVLPEDLCHKFLQLAESNIVRGIIICGIL 297
AMSH SLAPGALSNESEIFPTIDGLRVVVVFORICQQLQASANTARGVETCGIL 285
      |*..* ..|. . .|***** **;* ** *****;..*|*****
AMSH1 CGK LITNKE FTITHVIVEKQSAGPDYCDMENVEE LFNVDQDHDLLITGNIL 332
AMSH2 CGK LITNKE FTITHVIVEKQSAGPDYCDMENVEE LFNVDQDHDLLITGNIL 347
AMSH CGK LITNKE FTITHVILIEKQSAGSDYCDMENVEE LFLIQDQQLITGNIL 335
      ****;|*****;|*****.* **; ..|..* ..|..* ..|..* ..|..*
AMSH1 TPTPTATFLSSVLEITHC SVQMLMPEAIAVCS FKHKDTGIFRLINAGML 382
AMSH2 TPTPTATFLSSVLEITHC SVQMLMPEAIAVCS FKHKDTGIFRLINAGML 397
AMSH TPTPTATFLSSVLEITHC SVQMLMPEAIAVCS FKFKDTGIFK LITDGLK 385
      *****|*****; ****; *****;|*****;..*|..* ..|..*
AMSH1 EVSACKKKGFHEHTEKPRFLSICKHV--LVKDINKIIVDLR----- 421
AMSH2 EVSACKKKGFHEHTEKPRFLSICKHV--LVKDINKIIVDLR----- 447
AMSH EISCKRKGHEHTEKPRFLSICKHV--LVKDINKIIVDLR----- 424
      *;*;*|*****;|* ..* ..| ..| ..| ..| ..|
AMSH1 -----
AMSH2 LIGISRSSSPSEQL 461
AMSH -----

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FIGURE 2

COP9_su5_Hs	VGRLENAIGWYHSHPGYGCWLSGIDVSTQMLNQGFQEPFVA--VVIDPTRTISAGKVNLG
COP9_su5_Dm	VGRMEHAGWYHSHPGYGCWLSGINVSTQMLNQGFQEPFVA--IVVDPVRTVSAGKVCILG
COP9_su5_At	AGRLENVVVGWYHSHPGYGCWLSGIDVSTQRLNQGFQEPFLA--VVIDPTRTISAGKVEIG
COP9_su5_Ce	EGRKBKVVVGWYHSHPGYGCWLSGIDVSTQTLNQGFQEPFVA--IVIDPLRTMSAGKVDIG
AF2198_Arcfu	LPIQMKVFQTVHSHSPSCRPSEEDLSLPTFRGKYHIIVCY--PYDEDSWKVCYNRKGEV
PH0451_Pyrho	MFHDESIKOTFHSHSPFPYPSEEDLMFFSKFGKIHIIAAF--PYDEDSVKAFDSEGREV
TVN1035_Thevo	KPIDFSLVGSVHSHPSGITTKPSEEDLMFSLTGKIHIIIVGY--PYNLKDYSAYDRSGNKV
MTH971_Meth	LPPFTGAVGSVHSHPCPVNLPSAADLHFFSKNGLFHLIAH--PYTMETVAAYTRNGDPV
aq_1691_Aquae	ISKGMEIVGVYHSHPDHPRSQFDLQRAFPDLSYIIFSVQ--KGKVASYRSWELKGDKF
RV1334_Myctu	EDADEVVVVIYHSHTATEAYPSRTDVKLATEPDAHYVLVSTRDPHRHELRSYRIVDGAVT
RadC_Ecoli	IKINASALILAHNHPSCCARPSCADKLITERIIKSCQFMDL--RVLDHIVIGRGEYVSFA

.....HSHP'.....S''D

FIGURE 3

COP9_su5_Hs VGRLENAIGWYHSHPGYGCWLSGIDVSTQMLNQCFQEPFVA--VVIDPRTTISAGKVNLG
 COP9_su5_Dm VGRMEHAVGWYHSHPGYGCWLSGINVSTQMLNCTYQEPFVA--IVVDPVRTVSAGKVCLG
 COP9_su5_At AGRLENVVGVYHSHPGYGCWLSGIDVSTQRLNQOQSEFLA--VVIDPRTVTSAGKVBIG
 COP9_su5_Ce EGRKEKVVGVYHSHPGYGCWLSGIDVSTQTLNOKPOEPFWA--IVIDPLRTMSAGKVDIG
 Pad1_Dm TGRPEMVVGWYHSHPGFGCWLSGVDINTQGSFEALSERAVA--VVVDPIQSVKG-KVVID
 Pad1_Hs TGRPEMVVGWYHSHPGFGCWLSGVDINTQGSFEALSERAVA--VVVDPIQSVKG-KVVID
 Sks1_Dd TGRDEIVIGWYHSHPGFGCWLSGVDINTQGSFEALQSRAVA--VVVDPIQSVRG-KVVID
 Pad1_Sc TGRDQMVVGWYHSHPGFGCWLSGVDINTQKSFEQLNSRAVA--VVVDPIQSVKG-KVVID
 HSHF''''''S 'D

FIGURE 4